

SEQUENCE LISTING

<110> UNIVERSITY OF ROCHESTER

<120> Hormone Response Element Binding
Transregulators

<130> 21108.0032P1

<150> 60/508,763

<151> 2003-10-03

<160> 84

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1

agaaca

6

<210> 2

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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aggtca

6

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<221> misc_feature

<222> 7,8,9

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agaacammmt gttct

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aggtcanagg tca

13

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<400> 5

aggtcatgac ct

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<400> 6

ggtcacggtg gcc

13

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<400> 7

ggtgaccttg acc

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<211> 13

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<400> 8

ggtcaaggcg atc

13

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<221> misc_feature
<222> 6,7,8
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<400> 9
ggtcannntg acc 13

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<400> 10
gggcatcgtg acc 13

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<223> Description of Artificial Sequence; note =
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<400> 11
ggtcgccagg acc 13

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<400> 12
ggtcaggctg gtc 13

<210> 13
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<400> 13
ggccgggctg acc 13

<210> 14
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<400> 14
ggccgggctg acc 13

<210> 15
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<400> 15
ggccacgatg aca 13

<210> 16
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<400> 16
ggtggccctg acc 13

<210> 17
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<400> 17
ggtcaagggtg acc 13

<210> 18
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ggtcacgggtg acc 13

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<400> 19
gcaggagctg acc 13

<210> 20
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<400> 20
ggtcagcgtg gcc 13

<210> 21
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<400> 21
aatcagactg act 13

<210> 22
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<400> 22
ggtcaggctg gtc 13

<210> 23
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<213> Artificial Sequence

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 1 5 10 15
 Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile
 20 25 30
 Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile
 35 40 45
 Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys
 50 55 60
 Tyr Glu Val Gly Met
 65

<210> 24
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
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<400> 24
 Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys
 1 5 10 15
 His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
 20 25 30
 Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile
 35 40 45
 Lys Arg Ser
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<210> 25
 <211> 70
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
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<400> 25
 Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His
 1 5 10 15
 Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
 20 25 30
 Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
 35 40 45
 Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
 50 55 60
 Cys Tyr Glu Val Gly Met
 65 70

<210> 26
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =

synthetic construct

<400> 26

Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val Arg
 1 5 10 15
 Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly
 20 25

<210> 27

<211> 74

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
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<400> 27

Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
 1 5 10 15
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
 20 25 30
 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
 35 40 45
 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
 50 55 60
 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala
 65 70

<210> 28

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 28

Arg Lys Thr Lys Lys Lys Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly
 1 5 10 15
 Val Ser Gln Glu Thr Ser Glu Asn Pro Gly Asn Lys Thr Ile Val Pro
 20 25 30
 Ala Thr Leu Pro Gln Leu Thr Pro Thr Gly Arg
 35 40

<210> 29

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 29

Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His
 1 5 10 15
 Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
 20 25 30

Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr
 35 40 45
 Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys
 50 55 60
 Cys Tyr Glu Ala Gly Met Thr Leu
 65 70

<210> 30

<211> 56

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =
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<400> 30

Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu
 1 5 10 15
 Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln Lys
 20 25 30
 Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu
 35 40 45
 Asn Val Leu Glu Ala Ile Ala Arg
 50 55

<210> 31

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
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<400> 31

Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His
 1 5 10 15
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
 20 25 30
 Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
 35 40 45
 Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Arg Lys
 50 55 60
 Cys Cys Gln Ala Gly Met Val Leu
 65 70

<210> 32

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 32

Gly Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val Val Arg Ala
 1 5 10 15
 Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro Asn Glu Ser
 20 25 30

Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln
 35 40 45

Leu Ile Pro Pro Leu
 50

<210> 33

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 33

Lys Asp Glu Leu Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
 1 5 10 15
 Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
 20 25 30
 Ile Gln Lys Asn Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly Lys
 35 40 45
 Cys Val Ile Asp Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg Phe
 50 55 60
 Lys Lys Cys Ile Tyr Val Gly Met
 65 70

<210> 34

<211> 63

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 34

Ala Thr Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys
 1 5 10 15
 Leu Ile Glu Glu Asn Arg Glu Lys Arg Arg Arg Glu Glu Leu Gln Lys
 20 25 30
 Ser Ile Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile
 35 40 45
 Lys Thr Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser
 50 55 60

<210> 35

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 35

Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His
 1 5 10 15
 Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr
 20 25 30

Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu
 35 40 45
 Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
 50 55 60
 Cys Leu Ala Met Gly Met
 65 70

<210> 36

<211> 59

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 36

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn
 1 5 10 15
 Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val
 20 25 30
 Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr
 35 40 45
 Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser
 50 55

<210> 37

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
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<400> 37

Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr His
 1 5 10 15
 Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser
 20 25 30
 Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile
 35 40 45
 Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys
 50 55 60
 Cys Phe Glu Val Gly Met Ser Lys
 65 70

<210> 38

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 38

Glu Ser Val Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys
 1 5 10 15

Pro Glu Cys Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu
 20 25 30
 Ile Glu Lys Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys
 35 40 45
 Gln Leu Gly Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser
 50 55 60
 Leu Asp Ile Asp Leu
 65

<210> 39

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 39

Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr Gly Phe His Phe Asn
 1 5 10 15
 Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Met Lys
 20 25 30
 Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly Asp Cys Arg Ile Thr
 35 40 45
 Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg Leu Lys Arg Cys Val
 50 55 60
 Asp Ile Gly Met Met Lys
 65 70

<210> 40

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 40

Glu Phe Ile Leu Thr Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile
 1 5 10 15
 Leu Lys Arg Lys Glu Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys
 20 25 30
 Leu Ser Glu Glu Gln Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His
 35 40 45
 His Lys Thr Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro
 50 55 60
 Pro
 65

<210> 41

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 41

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Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
 1           5           10           15
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
          20           25           30
Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
      35           40           45
Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
      50           55           60
Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
65           70           75           80
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
          85           90           95
Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
          100          105          110
Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
      115          120          125
Leu Leu Ser Gln Ile Ser
      130

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<210> 42

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

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Lys Val Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu
 1           5           10           15
Asp Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe
          20           25           30
Asp Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr
      35           40           45
Pro His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu
      50           55           60
Phe Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly
65           70           75           80
Glu Phe Pro Gly Ile Arg Arg
          85

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<210> 43

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

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Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
 1           5           10           15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
          20           25           30
Met Leu Pro
      35

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<210> 44
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence; note =
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<400> 44
 Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe
 1 5 10 15
 Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
 20 25 30
 Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
 35 40 45
 Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
 50 55 60
 Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
 65 70 75 80
 Gln Glu Thr His Pro Asp Ser Glu Thr Ala
 85 90

<210> 45
 <211> 595
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
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<400> 45
 Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
 1 5 10 15
 Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
 20 25 30
 Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
 35 40 45
 Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
 50 55 60
 Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
 65 70 75 80
 Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
 85 90 95
 Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
 100 105 110
 Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
 115 120 125
 Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
 130 135 140
 Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
 145 150 155 160
 Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
 165 170 175
 Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
 180 185 190
 Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
 195 200 205
 Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
 210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
 225 230 235 240
 Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
 245 250 255
 Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
 260 265 270
 Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
 275 280 285
 Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
 290 295 300
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
 305 310 315 320
 Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
 325 330 335
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
 340 345 350
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
 355 360 365
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
 370 375 380
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
 385 390 395 400
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
 405 410 415
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
 420 425 430
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
 435 440 445
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
 450 455 460
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
 485 490 495
 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
 500 505 510
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
 515 520 525
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
 530 535 540
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
 545 550 555 560
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
 565 570 575
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
 580 585 590
 Ala Thr Val
 595

<210> 46

<211> 2092

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence; note =
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accggaccgc	caggctcccg	gggcagggcc	ggggccagag	ctcgcggtgc	ggcgggacat	180
gcgctgcgtc	gcctctaacc	tcgggctgtg	ctctttttcc	aggtggcccc	ccggtttctg	240
agcctttctg	cctgcgggga	cacgggtctg	accctgcccc	cggccacgga	ccatgaccat	300
gaccctccac	accaaagcat	ctgggatggc	cctactgcat	cagatccaag	ggaacgagct	360
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cctggacagc	agcaagcccc	cgtgtataaa	ctaccccag	ggcgccgcct	acgagttcaa	480
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ggccggcccc	ccggcattct	acaggccaaa	ttcagataat	cgacgccagg	gtggcagaga	780
aagattggcc	agtaccaatg	acaagggaag	tatggctatg	gaatctgcca	aggagactcg	840
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gggctgcaag	gccttcttca	agagaagtat	tcaaggacat	aacgactata	tgtgtccagc	960
caccaaccag	tgcaccattg	ataaaaaacg	gaggaagagc	tgccaggcct	gccggctccg	1020
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agacactttg	atccacctga	tggccaaggc	aggcctgacc	ctgcagcagc	agcaccagcg	1800
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gcatctgtac	agcatgaagt	gcaagaacgt	ggtgccccct	tatgacctgc	tgctggagat	1920
gctggacgcc	caccgcctac	atgcgcccac	tagccgtgga	ggggcatccg	tggaggagac	1980
ggaccaaagc	cacttggcca	ctgcgggctc	tacttcatcg	cattccttgc	aaaagtatta	2040
catcacgggg	gaggcagagg	gtttccctgc	cacagtctga	gagctccctg	gc	2092

<210> 47

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 47

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tgtgagggtc	gcaaggcctt	cttcaagaga	agtattcaag	gacataacga	ctatatgtgt	120
ccagccacca	accagtgcac	cattgataaa	aacaggagga	agagctgcca	ggcctgccgg	180
ctccgcaaat	gctacgaagt	gggaatg				207

<210> 48

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 48

atgaaagggtg	ggatacga	agaccgaaga	ggagggagaa	tgttgaaaca	caagcgccag	60
agagatgatg	gggagggcag	gggtgaagtg	gggtctgctg	gagacatgag	agctgccaac	120

ctttggccaa gcccgctcat gatcaaacgc tct

153

<210> 49

<211> 530

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 49

Met	Asp	Ile	Lys	Asn	Ser	Pro	Ser	Ser	Leu	Asn	Ser	Pro	Ser	Ser	Tyr	1	5	10	15
Asn	Cys	Ser	Gln	Ser	Ile	Leu	Pro	Leu	Glu	His	Gly	Ser	Ile	Tyr	Ile	20	25	30	
Pro	Ser	Ser	Tyr	Val	Asp	Ser	His	His	Glu	Tyr	Pro	Ala	Met	Thr	Phe	35	40	45	
Tyr	Ser	Pro	Ala	Val	Met	Asn	Tyr	Ser	Ile	Pro	Ser	Asn	Val	Thr	Asn	50	55	60	
Leu	Glu	Gly	Gly	Pro	Gly	Arg	Gln	Thr	Thr	Ser	Pro	Asn	Val	Leu	Trp	65	70	75	80
Pro	Thr	Pro	Gly	His	Leu	Ser	Pro	Leu	Val	His	Arg	Gln	Leu	Ser		85	90	95	
His	Leu	Tyr	Ala	Glu	Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	100	105	110	
Leu	Glu	His	Thr	Leu	Pro	Val	Asn	Arg	Glu	Thr	Leu	Lys	Arg	Lys	Val	115	120	125	
Ser	Gly	Asn	Arg	Cys	Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	130	135	140	
Asp	Ala	His	Phe	Cys	Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	145	150	155	160
Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	165	170	175	
Ile	Gln	Gly	His	Asn	Asp	Tyr	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	180	185	190	
Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	195	200	205	
Cys	Tyr	Glu	Val	Gly	Met	Val	Lys	Cys	Gly	Ser	Arg	Arg	Glu	Arg	Cys	210	215	220	
Gly	Tyr	Arg	Leu	Val	Arg	Gln	Arg	Ser	Ala	Asp	Glu	Gln	Leu	His		225	230	235	240
Cys	Ala	Gly	Lys	Ala	Lys	Arg	Ser	Gly	Gly	His	Ala	Pro	Arg	Val	Arg	245	250	255	
Glu	Leu	Leu	Leu	Asp	Ala	Leu	Ser	Pro	Glu	Gln	Leu	Val	Leu	Thr	Leu	260	265	270	
Leu	Glu	Ala	Glu	Pro	Pro	His	Val	Leu	Ile	Ser	Arg	Pro	Ser	Ala	Pro	275	280	285	
Phe	Thr	Glu	Ala	Ser	Met	Met	Ser	Leu	Thr	Lys	Leu	Ala	Asp	Lys		290	295	300	
Glu	Leu	Val	His	Met	Ile	Ser	Trp	Ala	Lys	Lys	Ile	Pro	Gly	Phe	Val	305	310	315	320
Glu	Leu	Ser	Leu	Phe	Asp	Gln	Val	Arg	Leu	Leu	Glu	Ser	Cys	Trp	Met	325	330	335	
Glu	Val	Leu	Met	Met	Gly	Leu	Met	Trp	Arg	Ser	Ile	Asp	His	Pro	Gly	340	345	350	
Lys	Leu	Ile	Phe	Ala	Pro	Asp	Leu	Val	Leu	Asp	Arg	Asp	Glu	Gly	Lys	355	360	365	
Cys	Val	Glu	Gly	Ile	Leu	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Thr	370	375	380	

Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
 385 390 395 400
 Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
 405 410 415
 Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
 420 425 430
 Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
 435 440 445
 Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
 450 455 460
 Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
 465 470 475 480
 Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
 485 490 495
 Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
 500 505 510
 Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
 515 520 525
 Ser Gln
 530

<210> 50

<211> 2011

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 50

tttcagtttc	tccagctgct	ggcttttttg	acaccactc	ccccgccagg	aggcagttgc	60
aagcgcgagg	gctgcgagaa	ataactgcct	cttgaaactt	gcagggcgaa	gagcaggcgg	120
cgagcgctgg	gccggggagg	gaccaccoga	gctgcgacgg	gctctggggc	tgcggggcag	180
ggctggcgcc	cggagcctga	gctgcaggag	gtgcgctcgc	tttctcaac	aggtggcggc	240
ggggcgcgcg	ccgggagacc	ccccctaata	cgggaaaagc	acgtgtccgc	attttagaga	300
aggcaaggcc	ggtgtgttta	tctgcaagcc	attatacttg	cccacgaatc	tttgagaaca	360
ttataatgac	ctttgtgcct	cttcttgcaa	ggtgttttct	cagctgttat	ctcaagacat	420
ggatataaaa	aactcaccat	ctagccttaa	ttctccttcc	tcctacaact	gcagtcaatc	480
catcttacct	ctggagcacg	gctccatata	cataccttcc	tcctatgtag	acagccacca	540
tgaatatcca	gccatgacat	tctatagccc	tgctgtgatg	aattacagca	ttcccagcaa	600
tgtcactaac	ttggaagggt	ggcctgggtcg	gcagaccaca	agcccaaata	tgttgtggcc	660
aacacctggg	cacctttctc	cttttagtgg	ccatcgccag	ttatcacatc	tgtatgcgga	720
acctcaaaaag	agtccttggt	gtgaagcaag	atcgctagaa	cacaccttac	ctgtaaacag	780
agagacactg	aaaaggaagg	ttagtgggaa	ccgttgcgcc	agccctgtta	ctgggtccagg	840
ttcaaagagg	gatgctcact	tctgcgctgt	ctgcagcgat	tacgcacg	gatataccta	900
tggagtctgg	tcgtgtgaag	gatgtaaggc	cttttttaaa	agaagcattc	aaggacataa	960
tgattatatt	tgtccagcta	caaatacagt	tacaatcgat	aaaaaccggc	gcaagagctg	1020
ccaggcctgc	cgacttcgga	agtgttacga	agtgggaatg	gtgaagtgtg	gctcccggag	1080
agagagatgt	gggtaccgcc	ttgtgcggag	acagagaagt	gccgacgagc	agctgcaactg	1140
tgccggcaag	gccaagagaa	gtggcgggcca	cgcgccccga	gtgcgggagc	tgctgctgga	1200
cgccctgagc	cccagagcagc	tagtgctcac	cctcctggag	gctgagccgc	cccatgtgct	1260
gatcagccgc	cccagtgcgc	ccttcaccga	ggcctccatg	atgatgtccc	tgaccaagtt	1320
ggccgacaag	gagttggtac	acatgatcag	ctggggccaag	aagattcccg	gctttgtgga	1380
gctcagcctg	ttcgaccaag	tgcggctctt	ggagagctgt	tggatggagg	tgtaaatgat	1440
ggggctgatg	tggcgctcaa	ttgaccaccc	cggcaagctc	atctttgtct	cagatcttgt	1500
tctggacagg	gatgagggga	aatgcgtaga	aggaattctg	gaaatctttg	acatgctcct	1560
ggcaactact	tcaaggtttc	gagagttaaa	actccaacac	aaagaatatc	tctgtgtcaa	1620
ggccatgatc	ctgctcaatt	ccagtatgta	ccctctgggc	acagcgaccc	aggatgctga	1680
cagcagccgg	aagctggctc	acttgctgaa	cgcctggacc	gatgctttgg	tttgggtgat	1740
tgccaagagc	ggcatctcct	cccagcagca	atccatgcgc	ctggctaacc	tcctgatgct	1800

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cctgtccac gtcaggcatg cgagtaacaa gggcatggaa catctgctca acatgaagtg 1860
caaaaatgtg gtcccagtgt atgacctgct gctggagatg ctgaatgccc acgtgcttcg 1920
cgggtgcaag tcctccatca cgggggccga gtgcagcccg gcagaggaca gtaaaagcaa 1980
agagggtccc cagaaccac agtctcagt a 2011

```

<210> 51
 <211> 210
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 51
gatgtcact tctgcgctgt ctgcagcgat tacgcatcgg gatatcacta tggagtctgg 60
tcgtgtgaag gatgtaaggc cttttttaaa agaagcattc aaggacataa tgattatatt 120
tgtccagcta caaatcagtg tacaatcgat aaaaaccggc gcaagagctg ccaggcctgc 180
cgacttcgga agtggtacga agtggggaatg 210

```

<210> 52
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 52
gtgaagtgtg gctcccggag agagagatgt gggtagcgcc ttgtgcggag acagagaagt 60
gccgacgagc agctgcactg tgccggc 87

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<210> 53
 <211> 777
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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<400> 53
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1      5      10      15
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20      25      30
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35      40      45
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50      55      60
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65      70      75      80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85      90      95
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100     105     110
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115     120     125
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130     135     140

```

Thr	Ala	Val	Ser	Ala	Ala	Pro	Thr	Glu	Lys	Glu	Phe	Pro	Lys	Thr	His
145					150					155					160
Ser	Asp	Val	Ser	Ser	Glu	Gln	Gln	His	Leu	Lys	Gly	Gln	Thr	Gly	Thr
				165					170						175
Asn	Gly	Gly	Asn	Val	Lys	Leu	Tyr	Thr	Thr	Asp	Gln	Ser	Thr	Phe	Asp
			180					185					190		
Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr
		195					200					205			
Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu
	210					215					220				
Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn
225				230						235					240
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys
			245						250					255	
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr
		260						265					270		
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr
	275						280					285			
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala
	290					295					300				
Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser
305				310						315					320
Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met
			325						330					335	
Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn
		340						345					350		
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln
	355						360					365			
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro
	370					375					380				
Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro
385				390						395					400
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro
			405						410					415	
Pro	Pro	Lys	Leu	Cys	Leu	Val	Cys	Ser	Asp	Glu	Ala	Ser	Gly	Cys	His
		420						425					430		
Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala
	435					440					445				
Val	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp	Cys	Ile
	450					455					460				
Ile	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Tyr	Arg	Lys
465				470						475					480
Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys	Lys	Lys
			485						490					495	
Ile	Lys	Gly	Ile	Gln	Gln	Ala	Thr	Thr	Gly	Val	Ser	Gln	Glu	Thr	Ser
		500						505					510		
Glu	Asn	Pro	Gly	Asn	Lys	Thr	Ile	Val	Pro	Ala	Thr	Leu	Pro	Gln	Leu
	515					520						525			
Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu
	530					535					540				
Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met
545				550						555					560
Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys
			565						570					575	
Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Arg	Asn	Leu	His	Leu	Asp	Asp	Gln
		580						585					590		
Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	Met	Phe	Leu	Met	Ala	Phe	Ala	Leu
	595					600						605			
Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala
	610					615					620				

```

Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
625                      630                      635                      640
Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
                      645                      650                      655
Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu Leu
                      660                      665                      670
Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
                      675                      680                      685
Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
                      690                      695                      700
Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705                      710                      715                      720
Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
                      725                      730                      735
Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
                      740                      745                      750
Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
                      755                      760                      765
Ile Lys Lys Leu Leu Phe His Gln Lys
770                      775

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<210> 54

<211> 4788

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 54

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tttttagaaa aaaaaaatat atttccctcc tgctccttct gcgttcacaa gctaagttgt      60
ttatctcggc tgcggcggga actgcgagcg gtggcgggag agcggctcct ctgccagagt      120
tgatattcac tgatggactc caaagaatca ttaactcctg gtagagaaga aaacccagc      180
agtgtgcttg ctcaggagag gggagatgtg atggacttct ataaaaccct aagaggagga      240
gctactgtga aggtttctgc gtcttcaccc tcaactggctg tcgcttctca atcagactcc      300
aagcagcgaa gacttttggg tgattttcca aaaggctcag taagcaatgc gcagcagcca      360
gatctgtcca aagcagtttc actctcaatg ggactgtata tgggagagac agaaacaaaa      420
gtgatgggaa atgacctggg attcccacag cagggccaaa tcagcctttc ctcgggggaa      480
acagacttaa agcttttgga agaaagcatt gcaaacctca ataggtcgac cagtgttcca      540
gagaacccca agagttcagc atccactgct gtgtctgctg cccccacaga gaaggagttt      600
ccaaaaactc actctgatgt atcttcagaa cagcaacatt tgaagggcca gactggcacc      660
aacggtggga atgtgaaatt gtataccaca gaccaagca cctttgacat tttgcaggat      720
ttggagtttt cttctgggtc cccaggtaaa gagacgaatg agagtccttg gagatcagac      780
ctgttgatag atgaaaactg tttgctttct cctctggcgg gagaagacga ttcattcctt      840
ttggaaggaa actcgaatga ggactgcaag cctctcattt taccggacac taaacccaaa      900
attaaggata atggagatct ggttttgtca agccccagta atgtaacact gccccaagtg      960
aaaacagaaa aagaagattt catcgaactc tgcacccctg gggtaattaa gcaagagaaa     1020
ctgggcacag tttactgtca ggcaagcttt cctggagcaa atataattgg taataaaatg     1080
tctgccattt ctgttcatgg tgtgagtacc tctggaggac agatgtacca ctatgacatg     1140
aatacagcat ccctttctca acagcaggat cagaagccta tttttaatgt cattccacca     1200
attcccgttg gttccgaaaa ttggaatagg tgccaaggat ctggagatga caacttgact     1260
tctctgggga cctcgaactt ccctggctga acagtttttt ctaatggcta ttcaagcccc     1320
agcatgagac cagatgtaag ctctcctcca tccagctcct caacagcaac aacaggacca     1380
cctcccaaac tctgcctggg gtgctctgat gaagcttcag gatgtcatta tggagtctta     1440
acttgtggaa gctgtaaagt tttcttcaaa agagcagtgg aaggacagca caattaccta     1500
tgtgtctggaa ggaatgattg catcatcgat aaaattcgaa gaaaaaactg cccagcatgc     1560
cgctatcgaa aatgtcttca ggctggaatg aacctggaag ctcgaaaaaac aaagaaaaaa     1620
ataaaaggaa ttcagcaggc cactacagga gtctcacaag aaacctctga aaatcctggg     1680
aacaaaacaa tagttcctgc aacgttacca caactcacc ctaccctggg gtcactgttg     1740
gaggttattg aacctgaagt gttatatgca ggatatgata gctctgttcc agactcaact     1800

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tggaggatca	tgactacgct	caacatgtta	ggagggcggc	aagtgattgc	agcagtgaaa	1860
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cagtactcct	ggatgtttct	tatggcattt	gctctggggg	ggagatcata	tagacaatca	1980
agtgcacacc	tgctgtgttt	tgctcctgat	ctgattatta	atgagcagag	aatgactcta	2040
ccctgcatgt	acgaccaatg	taaacacatg	ctgtatgttt	cctctgagtt	acacaggcct	2100
caggatctct	atgaagagta	tctctgtatg	aaaaccttac	tgcttctctc	ttcagttcct	2160
aaggacgggc	tgaagagcca	agagctat	gatgaaatta	gaatgacct	catcaaagag	2220
ctaggaaaag	ccattgtcaa	gaggggaagg	aactccagcc	agaactggca	gcgggtttat	2280
caactgacaa	aactcttgga	ttctatgcat	gaagtgggtg	aaaatctcct	taactattgc	2340
ttccaaacat	ttttggataa	gaccatgagt	attgaattcc	ccgagatgtt	agctgaaatc	2400
atcaccaatc	agataccaaa	atattcaaat	ggaaatatca	aaaaacttct	gtttcatcaa	2460
aagtgactgc	cttaataaga	atgggtgcct	taaagaaagt	cgaattaata	gcttttattg	2520
tataaactat	cagtttgtcc	tgtagagggt	ttgttgtttt	attttttatt	gttttcatct	2580
gttgttttgt	tttaaatacg	cactacatgt	ggtttataga	gggccaagac	ttggcaacag	2640
aagcagttga	gtcgtcatca	cttttcagtg	atgggagagt	agatggtgaa	atttattagt	2700
taatataatcc	cagaaattag	aaacctta	atgtggacgt	aatctccaca	gtcaaagaag	2760
gatggcacct	aaaccaccag	tgcccaaagt	ctgtgtgatg	aactttctct	tcatactttt	2820
tttcacagtt	ggctggatga	aattttctag	actttctgtt	ggtgtatccc	ccccctgtat	2880
agttaggata	gcatttttga	tttatgcatg	gaaacctgaa	aaaaagttta	caagtgtata	2940
tcagaaaagg	gaagtgtg	cttttatagc	tattactgtc	tggttttaac	aatttccttt	3000
atatttagtg	aactacgctt	gctcattttt	tcttacataa	ttttttat	aagttattgt	3060
acagctgttt	aagatgggca	gctagttcgt	agctttccca	aataaactct	aaacattaat	3120
caatcatctg	tgtgaaaatg	ggttgggtgt	tctaacctga	tggcacttag	ctatcagaag	3180
accacaaaaa	ttgactcaaa	tctccagtat	tcttgtcaaa	aaaaaaaaaa	aaaaagctca	3240
tattttgtat	atatctgctt	cagtggagaa	ttatatagggt	tgtgcaaatt	aacagtccta	3300
actggtatag	agcacctagt	ccagtgaact	gctgggtaaa	ctgtggatga	tggttgcaaa	3360
agactaattt	aaaaaataac	taccaagagg	ccctgtctgt	acctaacgcc	ctatttttgc	3420
aatggctata	tggaagaaa	gctggtaaac	tatttgtctt	tcaggacctt	ttgaagtagt	3480
ttgtataact	tcttaaaagt	tgtgattcca	gataaccagc	tgtaacacag	ctgagagact	3540
tttaatcaga	caaagtaatt	cctctcacta	aactttaccc	aaaaactaaa	tctctaatat	3600
ggcaaaaatg	gctagacacc	catttttcaca	ttcccatctg	tcaccaattg	gttaatcttt	3660
cctgatggta	caggaaagct	cagctactga	tttttgtgat	ttagaactgt	atgtcagaca	3720
tccatgtttg	taaaactaca	catcccta	gtgtgccata	gagtttaaca	caagtcctgt	3780
gaatttcttc	actgttgaaa	attattttta	acaaaataga	agctgtagta	gccctttctg	3840
tgtgcacctt	accaactttc	tgtaaaactca	aaacttaaca	tattttactaa	gccacaagaa	3900
atltgatttc	tattcaagggt	ggccaaatta	tttgtgta	agaaaactga	aatcttaata	3960
ttaaaaatat	ggaacttcta	atataatttt	atatttagtt	atagtttcag	atatatatca	4020
tatttggtatt	cactaatctg	ggaagggaag	ggctactgca	gctttacatg	caatttatta	4080
aaatgattgt	aaaatagctt	gtatagtgt	aaataagaat	gattttttaga	tgagattgtt	4140
ttatcatgac	atgttatata	ttttttgtag	gggtcaaaga	aatgctgatg	gataacctat	4200
atgatttata	gtttgtacat	gcattcat	aggcagcgat	ggtctcagaa	accaaagct	4260
ttgctctagg	ggaagaggga	gatggagact	ggtcctgtgt	gcagtgaagg	ttgctgaggc	4320
tctgacctag	tgagattaca	gaggaagtta	tcctctgcct	cccatctga	ccacccttct	4380
cattccaaca	gtgagtctgt	cagcgcaggt	ttagtttact	caatctcccc	ttgactaaa	4440
gtatgtaaag	tatgtaaaca	ggagacagga	aggtgggtgct	tacatcctta	aaggcaccat	4500
ctaatagcgg	gttactttca	catacagccc	tccccagca	gttgaatgac	aacagaagct	4560
tcagaagttt	ggcaatagtt	tgcatagagg	taccagcaat	atgtaaata	tgagaatct	4620
cataggttgc	caataatata	ctaattcctt	tctatcctac	aacaagagtt	tatttccaaa	4680
taaaatgagg	acatgttttt	gttttctttg	aatgcttttt	gaatgttatt	tgttattttc	4740
agtatttttg	agaaattatt	taataaaaaa	acaatcattt	gctttttg		4788

<210> 55

<211> 222

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 55
 cctcccaaac tctgcttggt gtgctctgat gaagcttcag gatgtcatta tggagtctta 60
 acttggtgaa gctgtaaagt tttcttcaaa agagcagtg aaggacagca caattaccta 120
 tgtgctgaa ggaatgattg catcatcgat aaaattcgaa gaaaaaactg cccagcatgc 180
 cgctatcgaa aatgtcttca ggctggaatg aacctggaag ct 222

<210> 56
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 56
 cgaaaaacaa agaaaaaat aaaaggaatt cagcaggcca ctacaggagt ctcacaagaa 60
 acctctgaaa atcctggtaa caaaacaata gttcctgcaa cgttaccaca actcaccct 120
 acc 123

<210> 57
 <211> 734
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 57
 Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser
 1 5 10 15
 Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys
 20 25 30
 Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu
 35 40 45
 Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu
 50 55 60
 Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala
 65 70 75 80
 Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro
 85 90 95
 Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser
 100 105 110
 Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys
 115 120 125
 Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly
 130 135 140
 Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser
 145 150 155 160
 Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn
 165 170 175
 Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro His
 180 185 190
 Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala
 195 200 205
 Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu
 210 215 220
 His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala
 225 230 235 240

Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	
				245					250					255		
Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
			260					265						270		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
			275				280							285		
Ala	Glu	Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	
			290			295					300					
Ala	Gly	Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	
305					310					315					320	
Gly	Met	Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	
				325					330					335		
Glu	Met	Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	
			340					345						350		
Arg	Leu	Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	
			355				360						365			
Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	
			370			375					380					
His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	
385					390					395					400	
Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	
				405					410					415		
Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	
			420					425						430		
Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	
			435				440						445			
Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	
			450			455					460					
Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	
465					470					475					480	
Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	
				485					490					495		
Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	
				500				505					510			
Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	
			515				520						525			
His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	
			530			535					540					
Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	
545					550					555					560	
Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	
				565					570					575		
Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	
			580					585					590			
Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	
			595				600					605				
Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	
			610			615					620					
Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	
625					630					635					640	
Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	
				645					650					655		
Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	
			660					665					670			
Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	
			675				680					685				
His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	
			690			695					700					
Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	
705					710					715					720	

Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln
725 730

<210> 58
<211> 2205
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 58
atgcaactcc ttcagcaaca gcagcaggaa gcagtatccg aaggcagcag cagcgggaga 60
gcgagggagg cctcgggggc tcccacttcc tccaaggaca attacttagg gggcacttcg 120
accatttctg acaacgcaa ggagtttgtt aaggcagtgt cgggtgtccat gggcctgggt 180
gtggaggcgt tggagcatct gagtccagg gaacagcttc ggggggattg catgtacgcc 240
ccacttttgg gaggttccacc cgctgtgcgt cccactcctt gtgccccatt ggccgaatgc 300
aaaggttctc tgctagacga cagcgcaggc aagagcactg aagatactgc tgagtattcc 360
cctttcaagg gaggttacac caaagggcta gaaggcgaga gcctaggctg ctctggcagc 420
gctgcagcag ggagctccgg gacacttgaa ctgccgtcta ccctgtctct ctacaagtcc 480
ggagcactgg acgaggcagc tgcgtaccag agtcgcgact actacaactt tccactggct 540
ctggccggac cgccgcccc tccgcgcct ccccatcccc acgctcgcac caagctggag 600
aaccgcgtgg actacggcag cgcttgggag gctgcggcgg cgagtgccg ctatggggac 660
ctggcgagcc tgcattggcg ggggtgcagc ggaccgggt ctgggtcacc ctgagccgcc 720
gcttctctat cctggcacac tctcttcaca gccgaagaag gccagttgta tggaccgtgt 780
gggtgggtgg ggggtgggtg tggcgggcgg gggcgggcgg gggcgggcgg cgggcgggc 840
ggcgggcgcg gcggcgggcg cgaggcgga gctgtagccc cctacggcta cactcggccc 900
cctcaggggc tggcgggcca ggaaagcgac ttcaccgcac ctgatgtgtg gtaccctggc 960
ggcatggtga gcagagtgcc ctatcccagt cccacttgtg tcaaaagcga aatgggcccc 1020
tggatggata gctactccgg accttacggg gacatgcgtt tggagactgc cagggaccat 1080
gttttgccca ttgactatta ctttccaccc cagaagacct gcctgatctg tggagatgaa 1140
gcttctgggt gtcactatgg agctctcaca tgtggaagct gcaaggctct cttcaaaaga 1200
gccgctgaag ggaaacagaa gtacctgtgc gccagcagaa atgattgcac tattgataaa 1260
ttccgaagga aaaattgtcc atcttgcgt cttcggaat gttatgaagc agggatgact 1320
ctgggagccc ggaagctgaa gaaacttggg aatctgaaac tacaggagga aggagaggct 1380
tccagcacca ccagccccac tgaggagaca acccagaagc tgacagtgtc acacattgaa 1440
ggctatgaat gtcagcccat ctttctgaat gtccgtggaag ccattgagcc aggtgtagtg 1500
tgtgctggac acgacaacaa ccagcccgac tcctttgcag ccttgctctc tagcctcaat 1560
gaactgggag agagacagct tgtacacgtg gtcaagtggg ccaaggcctt gcctggcttc 1620
cgcaacttac acgtggacga ccagatggct gtcattcagt actcctggat ggggctcatg 1680
gtgtttgcca tgggctggcg atccttcacc aatgtcaact ccaggatgct ctacttcgcc 1740
cctgatctgg ttttcaatga gtaccgcac cacaagtccc ggatgtacag ccagtgtgtc 1800
cgaatgagga acctctctca agagtttggg tggctccaaa tcacccccca ggaattcctg 1860
tgcatgaaag cactgctact cttcagcatt attccagtgg atgggctgaa aaatcaaaaa 1920
ttctttgatg aacttcgaat gaactacatc aaggaactcg atcgatcat tgcattgcaa 1980
agaaaaaatc ccacatcctg ctcaagacgc ttctaccagc tcaccaagct cctggactcc 2040
gtgcagccta ttgcgagaga gctgcacatc ttcacttttg acctgctaata caagtcacac 2100
atgggtgagc tggactttcc ggaaatgatg gcagagatca tctctgtgca agtgcccaag 2160
atcctttctg ggaaagtcaa gcccatctat ttccacaccc agtga 2205

<210> 59
<211> 216
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 59
 cccagaaga cctgcctgat ctgtggagat gaagcttctg ggtgtcacta tggagctctc 60
 acatgtggaa gctgcaagggt cttcttcaaa agagccgctg aagggaaca gaagtacctg 120
 tgcgccagca gaaatgattg cactattgat aaattccgaa ggaaaaattg tccatcttgt 180
 cgtcttcgga aatgttatga agcagggatg actctg 216

<210> 60
 <211> 162
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 60
 ggagcccga agctgaagaa acttggtaat ctgaaactac aggaggaagg agaggcttcc 60
 agcaccacca gccccactga ggagacaacc cagaagctga cagtgtcaca cattgaaggc 120
 tatgaatgtc agcccatctt tctgaatgtc ctggaagcca tt 162

<210> 61
 <211> 933
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 61
 Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
 1 5 10 15
 Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
 20 25 30
 Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
 35 40 45
 Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
 50 55 60
 Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
 65 70 75 80
 Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95
 Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110
 Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125
 Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140
 Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160
 Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175
 Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190
 Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205
 Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220
 Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240

Pro	Arg	Ala	Leu	Gly	Gly	Ala	Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Val			
				245					250					255				
Pro	Pro	Gly	Ala	Ala	Ala	Gly	Gly	Val	Ala	Leu	Val	Pro	Lys	Glu	Asp			
		260						265					270					
Ser	Arg	Phe	Ser	Ala	Pro	Arg	Val	Ala	Leu	Val	Glu	Gln	Asp	Ala	Pro			
		275					280						285					
Met	Ala	Pro	Gly	Arg	Ser	Pro	Leu	Ala	Thr	Thr	Val	Met	Asp	Phe	Ile			
	290					295					300							
His	Val	Pro	Ile	Leu	Pro	Leu	Asn	His	Ala	Leu	Leu	Ala	Ala	Arg	Thr			
305					310					315					320			
Arg	Gln	Leu	Leu	Glu	Asp	Glu	Ser	Tyr	Asp	Gly	Gly	Ala	Gly	Ala	Ala			
				325					330					335				
Ser	Ala	Phe	Ala	Pro	Pro	Arg	Ser	Ser	Pro	Cys	Ala	Ser	Ser	Thr	Pro			
		340					345						350					
Val	Ala	Val	Gly	Asp	Phe	Pro	Asp	Cys	Ala	Tyr	Pro	Pro	Asp	Ala	Glu			
		355					360					365						
Pro	Lys	Asp	Asp	Ala	Tyr	Pro	Leu	Tyr	Ser	Asp	Phe	Gln	Pro	Pro	Ala			
	370					375					380							
Leu	Lys	Ile	Lys	Glu	Glu	Glu	Glu	Gly	Ala	Glu	Ala	Ser	Ala	Arg	Ser			
385					390					395					400			
Pro	Arg	Ser	Tyr	Leu	Val	Ala	Gly	Ala	Asn	Pro	Ala	Ala	Phe	Pro	Asp			
				405					410					415				
Phe	Pro	Leu	Gly	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Arg	Ala	Thr	Pro	Ser			
		420					425						430					
Arg	Pro	Gly	Glu	Ala	Ala	Val	Thr	Ala	Ala	Pro	Ala	Ser	Ala	Ser	Val			
		435					440					445						
Ser	Ser	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Leu	Glu	Cys	Ile	Leu	Tyr	Lys			
	450					455					460							
Ala	Glu	Gly	Ala	Pro	Pro	Gln	Gln	Gly	Pro	Phe	Ala	Pro	Pro	Pro	Cys			
465					470					475					480			
Lys	Ala	Pro	Gly	Ala	Ser	Gly	Cys	Leu	Leu	Pro	Arg	Asp	Gly	Leu	Pro			
				485					490					495				
Ser	Thr	Ser	Ala	Ser	Ala	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Ala	Leu	Tyr			
		500					505						510					
Pro	Ala	Leu	Gly	Leu	Asn	Gly	Leu	Pro	Gln	Leu	Gly	Tyr	Gln	Ala	Ala			
		515					520						525					
Val	Leu	Lys	Glu	Gly	Leu	Pro	Gln	Val	Tyr	Pro	Pro	Tyr	Leu	Asn	Tyr			
	530					535						540						
Leu	Arg	Pro	Asp	Ser	Glu	Ala	Ser	Gln	Ser	Pro	Gln	Tyr	Ser	Phe	Glu			
545					550					555					560			
Ser	Leu	Pro	Gln	Lys	Ile	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly			
				565					570					575				
Cys	His	Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys			
		580						585					590					
Arg	Ala	Met	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp			
		595					600						605					
Cys	Ile	Val	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Leu			
	610					615					620							
Arg	Lys	Cys	Cys	Gln	Ala	Gly	Met	Val	Leu	Gly	Gly	Arg	Lys	Phe	Lys			
625					630					635					640			
Lys	Phe	Asn	Lys	Val	Arg	Val	Val	Arg	Ala	Leu	Asp	Ala	Val	Ala	Leu			
				645					650					655				
Pro	Gln	Pro	Val	Gly	Val	Pro	Asn	Glu	Ser	Gln	Ala	Leu	Ser	Gln	Arg			
		660					665						670					
Phe	Thr	Phe	Ser	Pro	Gly	Gln	Asp	Ile	Gln	Leu	Ile	Pro	Pro	Leu	Ile			
		675					680					685						
Asn	Leu	Leu	Met	Ser	Ile	Glu	Pro	Asp	Val	Ile	Tyr	Ala	Gly	His	Asp			
	690					695					700							
Asn	Thr	Lys	Pro	Asp	Thr	Ser	Ser	Ser	Leu	Leu	Thr	Ser	Leu	Asn	Gln			
705					710					715					720			

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
 725 730 735
 Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
 740 745 750
 Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
 755 760 765
 Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
 770 775 780
 Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr
 785 790 795 800
 Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu
 805 810 815
 Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu
 820 825 830
 Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
 835 840 845
 Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
 850 855 860
 Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
 865 870 875 880
 His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
 885 890 895
 Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
 900 905 910
 Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu
 915 920 925
 Leu Phe His Lys Lys
 930

<210> 62

<211> 3014

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 62

ctgaccagcg	ccgcccctccc	ccgcccccca	cccaggaggt	ggagatccct	ccggtccagc	60
cacattcaac	acccactttc	tcctccctct	gccctatat	tcccgaacc	ccctccctct	120
tcccttttcc	ctcctccctg	gagacggggg	aggagaaaag	gggagtccag	tcgtcatgac	180
tgagctgaag	gcaaagggtc	cccgggctcc	ccacgtggcg	ggcggcccg	cctccccga	240
ggtcggatcc	ccactgctgt	gtcgccagc	cgcaggtccg	ttcccgggga	gccagacctc	300
ggacaccttg	cctgaagttt	cggccatacc	tatctccctg	gacgggctac	tcttccctcg	360
gccctgccag	ggacaggacc	cctccgacga	aaagacgcag	gaccagcagt	cgctgtcgga	420
cgtggagggc	gcatattcca	gagctgaagc	tacaaggggt	gctggaggca	gcagttctag	480
tccccagaa	aaggacagcg	gactgctgga	cagtgtcttg	gacactctgt	tggcgccctc	540
aggtcccggg	cagagccaac	ccagccctcc	cgctgcgag	gtcaccagct	cttggtgctt	600
gtttggcccc	gaacttccc	aagatccacc	ggctgcccc	gccaccagc	gggtgtgtgc	660
cccgtcatg	agccgggtcc	ggtgcaagg	tggagacagc	tccgggacgg	cagctgcca	720
taaagtgtg	ccccggggcc	tgccaccagc	ccggcagctg	ctgctcccg	cctctgagag	780
ccctcactgg	tccggggccc	cagtgaagcc	gtctccgcag	gccgctgcgg	tggagggtga	840
ggaggaggat	ggctctgagt	ccgaggagtc	tgcgggtccg	cttctgaagg	gcaaacctcg	900
ggctctgggt	ggcgcgggcg	ctggaggagg	agccgcggct	gtcccgcgg	gggcggcagc	960
aggaggcgtc	gccctggtcc	ccaagggaag	ttcccgcctt	tcagcgccca	gggtcgccct	1020
ggtggagcag	gacgcgccga	tggcgccccg	gcgctccccg	ctggccacca	cggtgatgga	1080
tttcatccac	gtgcctatcc	tgcctctcaa	tcacgcctta	ttggcagccc	gcactcgcca	1140
gctgctggaa	gacgaaagtt	acgacggcg	ggccggggct	gccagcgcc	ttgccccgcc	1200
gcggagttca	ccctgtgcct	cgtccacccc	ggtcgctgta	ggcgacttcc	ccgactgcgc	1260
gtacccgccc	gacgccgagc	ccaaggacga	cgcgtaacct	ctctatagcg	acttccagcc	1320

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gcccgcctcta aagataaagg aggaggagga aggcgcggag gcctccgcgc gctccccgcg 1380
ttcctacctt gtggccgggtg ccaaccccg agccttcccc gatttcccgt tggggccacc 1440
gccccgcgtg ccgcccgcgag cgaccccatc cagaccggg gaagcggcgg tgacggccgc 1500
acccgccagt gcctcagtct cgtctgcgtc ctccctcgggg tcgaccctgg agtgcatcct 1560
gtacaaagcg gagggcgcgcg cgccccagca gggcccggtt gcgcccgcgc cctgcaaggc 1620
gccgggcgcg agcggtgtgc tgctcccgcg ggacggcctg ccctccacct ccgctctgc 1680
cgccgcgcgc ggggcggccc ccgcgctcta ccctgcactc ggcctcaacg ggctcccga 1740
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agggatgggt aaaccccttc tctttcataa aaagtgaatg tcattctttt cttttaaaga 3000
attaaatttt gtgg 3014

```

<210> 63
 <211> 216
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

```

<400> 63
cctcagaaga tttgtttaat ctgtggggat gaagcatcag gctgtcatta tgggtgtcctt 60
acctgtggga gctgtaagggt cttctttaag agggcaatgg aagggcagca caactactta 120
tgtgtcgga gaaatgactg catcgttgat aaaatccgca gaaaaaactg cccagcatgt 180
cgccctagaa agtgctgtca ggctggcatg gtcctt 216

```

<210> 64
 <211> 160
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

```

<400> 64
ggaggtcgaa aattttaaaa gttcaataaa gtcagagttg tgagagcact ggatgctggt 60
gctctccac agccagtggg cgttccaaat gaaagccaag ccctaagcca gagattcact 120
ttttcaccag gtcaagacat acagttgatt ccaccactga 160

```

<210> 65
 <211> 455

Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser
 420 425 430
 Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Leu Pro Pro
 435 440 445
 Leu Phe Glu Val Phe Glu Asp
 450 455

<210> 66
 <211> 1698
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 66
 cgggcggggat caactttgca tgaataatgt gagtgcgctt ggaaaagaga cctcctgctc 60
 cgcggggctcg gggcaagagc ccgcaggcta ccttccccgg gcagggggcgc tcaacccaac 120
 cggtccagg gcaactgtaa tttggctaga ggaccgcgcg gaggcagcgg gatctgcgat 180
 ttccttcttg ttggctgtcc tgcgtgggtg ccaagttcca cacatgattt aatgaataag 240
 aaggagatgt cagtgaaaaa agggatccag aatgattact aacctataac ccccaacagt 300
 atgacagaaa atggccttac agcttgggac aaaccgaagc actgtccaga ccgagaacac 360
 gactggaagc tagtaggaat gtctgaagcc tgcctacata ggaagagcca ttcagagagg 420
 cgcagcacgt tgaaaaatga acagtcgtcg ccacatctca tccagaccac ttggactagc 480
 tcaatattcc atctggacca tgatgatgtg aacgaccaga gtgtctcaag tgcccagacc 540
 ttccaaacgg aggagaagaa atgtaaaggg tacatcccca gttacttaga caaggacgag 600
 ctctgtgtag tgtgtggtga caaagccacc gggatcact accgctgtat cacgtgtgaa 660
 ggctgcaagg gtttcttttag aagaaccatt cagaaaaatc tccatccatc ctattcctgt 720
 aaatatgaag gaaaatgtgt catagacaaa gtcacgcgaa atcagtgccg ggaatgtcgc 780
 ttaagaaat gcatctatgt tggcatggca acagatttgg tgctggatga cagcaagagg 840
 ctggccaaga ggaagctgat agaggagaac cgggagaaaa gacggcggga agagctgcag 900
 aagtccatcg ggcacaagcc agagcccaca gacgaggaat gggagctcat caaaactgtc 960
 accgaagccc atgtggcgac caacgcccac ggagccact ggaagcaaaa accgaaat 1020
 ctgccagaag acattgggac agcaccaata gtcaatgcc cagaaggtgg aaaggttgac 1080
 ttggaagcct tcagccattt tacaaaaatc atcacaccag caattaccag agtgggtggat 1140
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 gagactttaa ccttgaatgg ggaaatggca gtgatacggg gccagctgaa aaatgggggt 1320
 cttgggggtg tgctcagacgc catctttgac ctaggcatgt ctctgtcttc tttcaacctg 1380
 gatgacactg aagtagccct ccttcaggcc gtccctgtga tgtcttcaga tcgcccgggg 1440
 cttgcctgtg ttgagagaat agaaaagtac caagatagtt tctgtctggc ctttgaacac 1500
 tatatcaatt accgaaaaca ccacgtgaca cacttttggc caaaactcct gatgaagggtg 1560
 acagatctgc ggatgatagg agcctgccat gccagccgct tcctgcacat gaagggtggaa 1620
 tgccccacag aactcctccc ccctttgttc ctggaagtgt tcgaggatta gactgactgg 1680
 attccttctc ataattcc 1698

<210> 67
 <211> 216
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 67
 aaggacgagc tctgtgtagt gtgtggtgac aaagccaccg ggtatcacta ccgctgtatc 60
 acgtgtgaag gctgcaaggg tttctttaga agaaccattc agaaaaatct ccatccatcc 120
 tattcctgta aatatgaagg aaaatgtgtc atagacaaag tcacgcgaaa tcagtgccag 180
 gaatgtcgct ttaagaaatg catctatgtt ggcgatg 216

<210> 68
 <211> 189
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 68
 gcaacagatt tgggtgctgga tgacagcaag aggctggcca agaggaagct gatagaggag 60
 aaccgggaga aaagacggcg ggaagagctg cagaagtcca tcgggcacaa gccagagccc 120
 acagacgagg aatgggagct catcaaaact gtcaccgaag cccatgtggc gaccaacgcc 180
 caaggcagc 189

<210> 69
 <211> 462
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 69
 Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
 1 5 10 15
 Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser
 20 25 30
 Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His
 35 40 45
 Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
 50 55 60
 Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
 65 70 75 80
 Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
 85 90 95
 Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
 100 105 110
 Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
 115 120 125
 Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
 130 135 140
 Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
 145 150 155 160
 Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
 165 170 175
 Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
 180 185 190
 Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
 195 200 205
 Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
 210 215 220
 Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
 225 230 235 240
 Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu
 245 250 255
 Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala
 260 265 270

Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His
 275 280 285
 Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly
 290 295 300
 Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val
 305 310 315 320
 Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser
 325 330 335
 Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu
 340 345 350
 Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly
 355 360 365
 Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser
 370 375 380
 Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu
 385 390 395 400
 Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala
 405 410 415
 Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys
 420 425 430
 Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp
 435 440 445
 Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr
 450 455 460

<210> 70

<211> 5449

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 70

gcgcgcggggg	ccgcgcgcgcc	cgccgccccgc	tgcctgcgcc	gccggccggg	catgagtttag	60
tcgcagacat	ggacaccaa	catttcctgc	cgctcgattt	ctccacccag	gtgaactcct	120
ccctcacctc	ccgcagggg	cgaggctcca	tggctgcccc	ctcgctgcac	ccgtccctgg	180
ggcctggcat	cggctccccg	ggacagctgc	attctcccat	cagcaccctg	agctccccca	240
tcaacggcat	gggcccgcct	ttctcggtca	tcagctcccc	catgggcccc	cactccatgt	300
cgggtgcccac	cacacccacc	ctgggcttca	gcactggcag	ccccagctc	agctcaccta	360
tgaaccccg	cagcagcagc	gaggacatca	agccccct	gggcctcaat	ggcgctctca	420
aggtccccgc	ccacccctca	ggaaacatgg	cttccttcac	caagcacatc	tgcgccatct	480
gcggggaccg	ctcctcaggc	aagcactatg	gagtgtacag	ctgcgagggg	tgcaagggct	540
tcttcaagcg	gacggtgcgc	aaggacctga	cctacacctg	ccgcgacaac	aaggactgcc	600
tgattgacaa	gcggcagcgg	aaccggtgcc	agtactgccc	ctaccagaag	tgcctggcca	660
tgggcatgaa	gcgggaagcc	gtgcaggagg	agcggcagcg	tggcaaggac	cggaaacgaga	720
atgaggtgga	gtcgaccagc	agcgccaacg	aggacatgcc	ggtggagagg	atcctggagg	780
ctgagctggc	cgtggagccc	aagaccgaga	cctacgtgga	ggcaaacatg	gggctgaacc	840
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gaaagcttcg	tccgagaaac	gccaggacag	acgatggcag	aggagagggc	tcctgtgacg	5100
gcggcgaggc	ttgggaggaa	accgccgcaa	tgggggtgtc	ttccctcggg	gcaggagggt	5160

```

gggcctgagg ctttcaaggg ttttcttccc tttcgagtaa tttttaaagc cttgctctgt      5220
tgtgtcctgt tgccggctct ggcccttctg tgactgactg tgaagtggct tctccgtacg      5280
attgtctctg aaacatcgtg gcctcagggtg ccagggtttg atggacagta gcattagaat      5340
tgtggaaaag gaacacgcaa agggagaaagt gtgagaggag aaacaaaata tgagcgttta      5400
aaatacatcg ccattcagtt cgttaaaaaa aaaaaaaaaa aaaaaaaaaa      5449

```

<210> 71
 <211> 210
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

```

<400> 71
accaagcaca tctgcgccat ctgcggggac cgctcctcag gcaagcacta tggagtgtac      60
agctgcgagg ggtgcaaggg cttcttcaag cggacggtgc gcaaggacct gacctacacc      120
tgccgcgaca acaaggactg cctgattgac aagcggcagc ggaaccggtg ccagtactgc      180
cgctaccaga agtgcctggc catgggcatg      210

```

<210> 72
 <211> 177
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

```

<400> 72
aagcggggaag ccgtgcagga ggagcggcag cgtggcaagg accggaacga gaatgagggtg      60
gagtcgacca gcagcgccaa cgaggacatg ccggtggaga ggatcctgga ggctgagctg      120
gccgtggagc ccaagaccga gacctacgtg gaggcaaaaca tggggctgaa ccccagc      177

```

<210> 73
 <211> 462
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

```

<400> 73
Met Ala Ser Asn Ser Ser Ser Cys Pro Thr Pro Gly Gly Gly His Leu
1      5      10      15
Asn Gly Tyr Pro Val Pro Pro Tyr Ala Phe Phe Phe Pro Pro Met Leu
20     25     30
Gly Gly Leu Ser Pro Pro Gly Ala Leu Thr Thr Leu Gln His Gln Leu
35     40     45
Pro Val Ser Gly Tyr Ser Thr Pro Ser Pro Ala Thr Ile Glu Thr Gln
50     55     60
Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro Pro Pro
65     70     75     80
Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys Ser Ser
85     90     95
Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly Phe Phe
100    105    110

```

Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg Asp Lys
 115 120 125
 Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr Cys Arg
 130 135 140
 Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val Arg Asn
 145 150 155 160
 Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys Ser Glu
 165 170 175
 Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys Val Arg
 180 185 190
 Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly Lys Tyr
 195 200 205
 Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile Asp Leu
 210 215 220
 Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys Thr Val
 225 230 235 240
 Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile Ala Asp
 245 250 255
 Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile Leu Arg
 260 265 270
 Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe Ser Asp
 275 280 285
 Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe Gly Pro
 290 295 300
 Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro Leu Glu
 305 310 315 320
 Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu Ile Cys
 325 330 335
 Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met Leu Gln
 340 345 350
 Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg Arg Pro
 355 360 365
 Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr Asp Leu
 370 375 380
 Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu Lys Met
 385 390 395 400
 Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu Glu Asn
 405 410 415
 Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly Gly Arg
 420 425 430
 Asp Gly Gly Gly Leu Ala Pro Pro Pro Gly Ser Cys Ser Pro Ser Leu
 435 440 445
 Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
 450 455 460

<210> 74

<211> 2907

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 74

gccatctggg	cccaggcccc	atgccccgag	gaggggtggt	ctgaagccca	ccagagcccc	60
ctgccagact	gtctgcctcc	cttctgactg	tggccgcttg	gcatggccag	caacagcagc	120
tcctgcccga	cacctggggg	cgggcacctc	aatgggtacc	cgggtgcctcc	ctacgccttc	180
ttcttcccc	ctatgctggg	tggactctcc	ccgccaggcg	ctctgaccac	tctccagcac	240
cagcttccag	ttagtggata	tagcacacca	tccccagcca	ccattgagac	ccagagcagc	300
agttctgaag	agatagtgcc	cagccctccc	tcgccacccc	ctctaccccg	catctacaag	360

ccttgctttg	tctgtcagga	caagtcctca	ggctaccact	atgggggtcag	cgctgtgag	420
ggctgcaagg	gcttcttccg	ccgcagcatc	cagaagaaca	tggtgtacac	gtgtcaccgg	480
gacaagaact	gcatcatcaa	caaggtgacc	cggaaaccgct	gccagtactg	ccgactgcag	540
aagtgccttg	aagtgggcat	gtccaaggag	tctgtgagaa	acgaccgaaa	caagaagaag	600
aaggagggtgc	ccaagcccga	gtgctctgag	agctacacgc	tgacgccgga	ggtgggggag	660
ctcattgaga	agggtgcgaa	agcgcaccag	gaaaccttcc	ctgccctctg	ccagctgggc	720
aaatacacta	cgaacaacag	ctcagaacaa	cgtgtctctc	tggacattga	cctctgggac	780
aagttcagtg	aactctccac	caagtgcata	attaagactg	tggagtctgc	caagcagctg	840
cccggcttca	ccaccctcac	catcgccgac	cagatcacc	tcctcaaggc	tgctgtcctg	900
gacatcctga	tcctgctggat	ctgcacgcgg	tacacgccc	agcaggacac	catgaccttc	960
tcggacgggc	tgacctgaa	ccggacccag	atgcacaacg	ctggcttcgg	ccccctcacc	1020
gacctgggtct	ttgccttcgc	caaccagctg	ctgcccctgg	agatggatga	tgccggagacg	1080
gggctgctca	gcgccatctg	cctcatctgc	ggagaccgcc	aggacctgga	gcagccggac	1140
cgggtggaca	tgctgcagga	gccgctgctg	gaggcgctaa	aggtctacgt	gcggaagcgg	1200
aggcccagcc	gccccacat	gttccccaa	atgctaata	agattactga	cctgcgaagc	1260
atcagcgcca	aggggtgta	gcgggtgatc	acgctgaaga	tggagatccc	gggctccatg	1320
ccgcctctca	tccaggaaat	gttggagaac	tcagagggcc	tggacactct	gagcggacag	1380
ccgggggggtg	gggggaggga	cggggggtggc	ctggccccc	cgccaggcag	ctgtagcccc	1440
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ccacatggac	acagccctcg	ccctccgccc	cggcttttct	ctgcctttct	accgaccatg	1560
tgaccccgca	ccagccctgc	ccccacctgc	cctcccgggc	agtactgggg	accttccctg	1620
ggggacgggg	agggaggagg	cagcgactcc	ttggacagag	gcctggggcc	tcagtggact	1680
gcctgtctcc	acagcctggg	ctgacgtcag	aggccgaggc	caggaactga	gtgaggcccc	1740
tggtctctgg	tctcaggatg	ggtcctgggg	gcctcgtggt	catcaagaca	ccctcttgcc	1800
cagctcacca	catcttcac	accagcaaac	ccaggactt	ggctccccc	tcctcagaac	1860
tcacaagcca	ttgctcccca	gctggggaac	ctcaacctcc	ccctgcctc	ggttggtgac	1920
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ggtattaatt	ctcgctgggt	ttgtttttat	tttaattttt	ttgttttgat	ttttttaata	2040
agaattttca	ttttaagcac	atttatactg	aaggaatttg	tgctgtgtat	tggggggagc	2100
tggatccaga	gctggagggg	gtgggtccgg	gggaggagg	ggctcggaag	gggccccac	2160
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gaagccgcca	gcccccttct	ccctctgcct	gacctggg	tgtggacggt	gtggggcagc	2340
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tcccgtcagg	gcccacatca	tctaggctcc	ccagcccca	ctgtgaagg	gctggccagg	2520
ggcccagact	gccccaccc	ccggcctcag	ccaccagcac	ccccatagg	ccccagaca	2580
ccacacacat	gcgcgtgcgc	acacacacaa	acacacacac	actggacagt	agatgggccg	2640
acacacactt	ggcccagagt	cctccatttc	cctggcctgc	ccccacccc	caacctgtcc	2700
cacccccgtg	ccccctcctt	accccgccag	acgggcctac	aggggggtct	cccctcaccc	2760
ctgcaccccc	agctggggga	gctggctctg	ccccgacctc	cttcaccagg	ggttggggcc	2820
ccttccccctg	gagcccgtgg	gtgcacctgt	tactgttggg	ctttccactg	agatctactg	2880
gataaagaat	aaagtctcat	ttattct				2907

<210> 75

<211> 216

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 75

atctacaagc	cttgctttgt	ctgtcaggac	aagtcctcag	gctaccacta	tgggggtcagc	60
gcctgtgagg	gctgcaagg	cttcttccgc	cgcagcatcc	agaagaacat	ggtgtacacg	120
tgccaccggg	acaagaactg	catcatcaac	aaggtgaccc	ggaaccgctg	ccagtactgc	180
cgactgcaga	agtgccttga	agtgggcatg	tccaag			216

<210> 76

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 76

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gagtcgtgta gaaacgaccg aaacaagaag aagaaggagg tgcccaagcc cgagtgtctct      60
gagagctaca cgctgacgcc ggaggtgggg gagctcattg agaaggtgcg caaagcgcac      120
caggaaacct tcctgccct ctgccagctg ggcaaataca ctacgaacaa cagctcagaa      180

caacgtgtct ctctggacat tgacctc      207

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<210> 77

<211> 427

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 77

```

Met Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly Asp Phe
 1          5          10          15
Asp Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg Ala Thr
          20          25          30
Gly Phe His Phe Asn Ala Met Thr Cys Glu Gly Cys Lys Gly Phe Phe
          35          40          45
Arg Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe Asn Gly
          50          55          60
Asp Cys Arg Ile Thr Lys Asp Asn Arg Arg His Cys Gln Ala Cys Arg
65          70          75          80
Leu Lys Arg Cys Val Asp Ile Gly Met Met Lys Glu Phe Ile Leu Thr
          85          90          95
Asp Glu Glu Val Gln Arg Lys Arg Glu Met Ile Leu Lys Arg Lys Glu
          100          105          110
Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu Glu Gln
          115          120          125
Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr Tyr Asp
          130          135          140
Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg Val Asn
145          150          155          160
Asp Gly Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His Thr Pro
          165          170          175
Ser Phe Ser Gly Asp Ser Ser Ser Ser Cys Ser Asp His Cys Ile Thr
          180          185          190
Ser Ser Asp Met Met Asp Ser Ser Ser Phe Ser Asn Leu Asp Leu Ser
          195          200          205
Glu Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser Gln Leu
          210          215          220
Ser Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile Gln Lys
225          230          235          240
Val Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu Thr Ser
          245          250          255
Glu Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val Ile Met
          260          265          270
Leu Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp Thr Cys
          275          280          285

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Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys Ala Gly
 290 295 300
 His Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val Gly Leu
 305 310 315 320
 Lys Lys Leu Asn Leu His Glu Glu Glu His Val Leu Leu Met Ala Ile
 325 330 335
 Cys Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala Leu Ile
 340 345 350
 Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr Ile Arg
 355 360 365
 Cys Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys Met Ile
 370 375 380
 Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn Glu Glu His Ser Lys Gln
 385 390 395 400
 Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu Thr Pro
 405 410 415
 Leu Val Leu Glu Val Phe Gly Asn Glu Ile Ser
 420 425

<210> 78

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 78

atggaggcaa	tggcggccag	cacttccctg	cctgaccctg	gagactttga	ccggaacgtg	60
ccccgatct	gtggggtgtg	tggagaccga	gccactggct	ttcacttcaa	tgctatgacc	120
tgtgaaggct	gcaaaggctt	cttcaggcga	agcatgaagc	ggaaggcact	attcacctgc	180
cccttcaacg	gggactgccg	catcaccaag	gacaaccgac	gccactgcca	ggcctgccgg	240
ctcaaacgct	gtgtggacat	cggcatgatg	aaggagttca	ttctgacaga	tgaggaagtg	300
cagaggaaagc	gggagatgat	cctgaagcgg	aaggaggagg	aggccttgaa	ggacagtctg	360
cggcccaagc	tgtctgagga	gcagcagcgc	atcattgcca	tactgctgga	cgccaccat	420
aagacctacg	acccaccta	ctccgaattc	tgccagttcc	ggcctccagt	tcgtgtgaat	480
gatggtggag	ggagccatcc	ttccaggccc	aactccagac	acactcccag	cttctctggg	540
gactcctcct	cctcctgctc	agatcactgt	atcacctctt	cagacatgat	ggactcgtcc	600
agcttctcca	atctggatct	gagtgaagaa	gattcagatg	acccttctgt	gaccctagag	660
ctgtcccagc	tctccatgct	gccccacctg	gctgacctgg	tcagttacag	catccaaaag	720
gtcattggct	ttgctaagat	gataccagga	ttcagagacc	tcacctctga	ggaccagatc	780
gtactgtctga	agtcaagtgc	cattgaggtc	atcatgttgc	gctccaatga	gtccttcacc	840
atggacgaca	tgtcctggac	ctgtggcaac	caagactaca	agtaccgcgt	cagtgcgtg	900
accaaagccg	gacacagcct	ggagctgatt	gagccctca	tcaagttcca	ggtgggactg	960
aagaagctga	acttgcata	ggaggagcat	gtcctgctca	tggccatctg	catcgtctcc	1020
ccagatcgtc	ctggggtgca	ggacgccgcg	ctgattgagg	ccatccagga	ccgcctgtcc	1080
aacacactgc	agacgtacat	ccgctgccgc	caccgcgcc	cgggcagcca	cctgctctat	1140
gccaaagatga	tccagaagct	agccgacctg	cgcagcctca	atgaggagca	ctccaagcag	1200
taccgctgcc	tctccttcca	gcctgagtgc	agcatgaagc	taacgcccct	tgtgctcgaa	1260
gtgtttggca	atgagatctc	ctga				1284

<210> 79

<211> 210

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 79
 cggatctgtg ggggtgtgtg agaccgagcc actggctttc acttcaatgc tatgacctgt 60
 gaaggctgca aaggcttctt caggcgaagc atgaagcgga aggcactatt cacctgcccc 120
 ttcaacgggg actgccgcat caccaaggac aaccgacgcc actgccaggc ctgccggctc 180
 aaacgctgtg tggacatcgg catgatgaag 210

<210> 80
 <211> 195
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 80
 gagttcattc tgacagatga ggaagtgcag aggaagcggg agatgatcct gaagcgggaag 60
 gaggaggagg ccttgaagga cagtctgcgg cccaagctgt ctgaggagca gcagcgcac 120
 attgccatac tgctggacgc ccaccataag acctacgacc ccacctactc cgacttctgc 180
 cagttccggc ctcca 195

<210> 81
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 81
 Met Lys Gly Gly Val Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys
 1 5 10 15
 His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
 20 25 30
 Ala Gly Asp Met Arg Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile
 35 40 45
 Lys Arg Ser
 50

<210> 82
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 82
 Met Ala Arg Arg Pro Arg His Ser Ile Tyr Ser Ser Asp Glu Asp Asp
 1 5 10 15
 Glu Asp Phe Glu Met Cys Asp His Asp Tyr Asp Gly Leu Leu Pro Lys
 20 25 30
 Ser Gly Lys Arg His Leu Gly Lys Thr Arg Trp Thr Arg Glu Glu
 35 40 45

<210> 83
 <211> 71
 <212> DNA
 <213> Artificial Sequence

